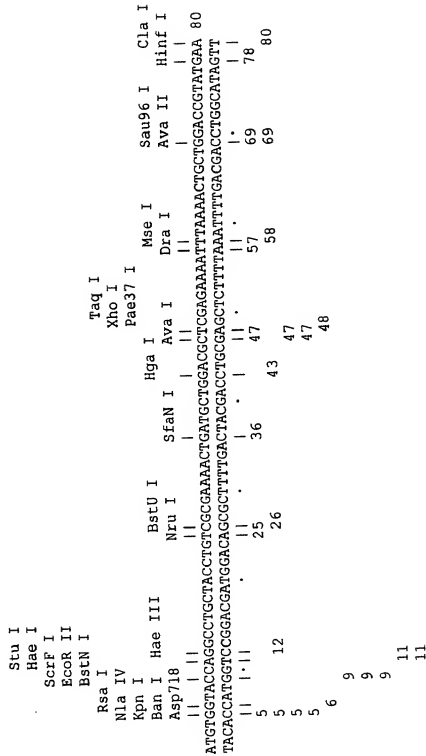
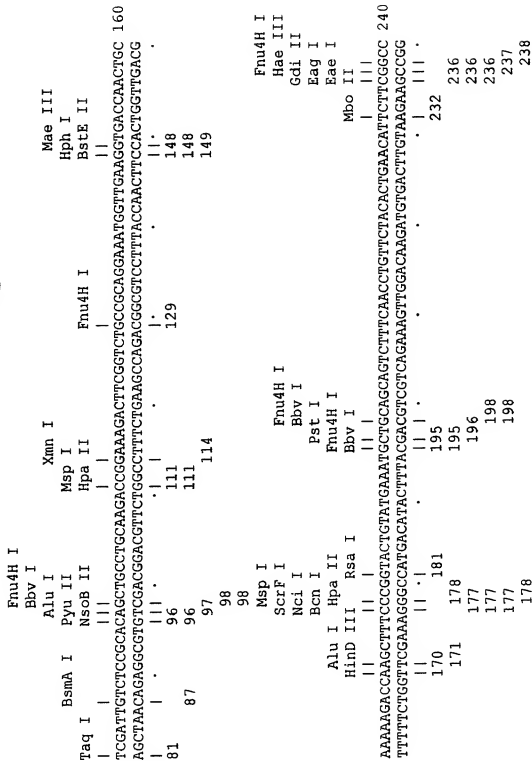


Fig. 1A

METOTP-1.SEQ4 -> Restriction Map

DNA sequence 540 b.p. ATGTGGTACCAG ... CCGTAGGTACC linear





Sau3A I
Mbo I
Sau3A I
Mbo I
Dpn I
Alw I
Nla IV

Fig. 1E

[illegible]

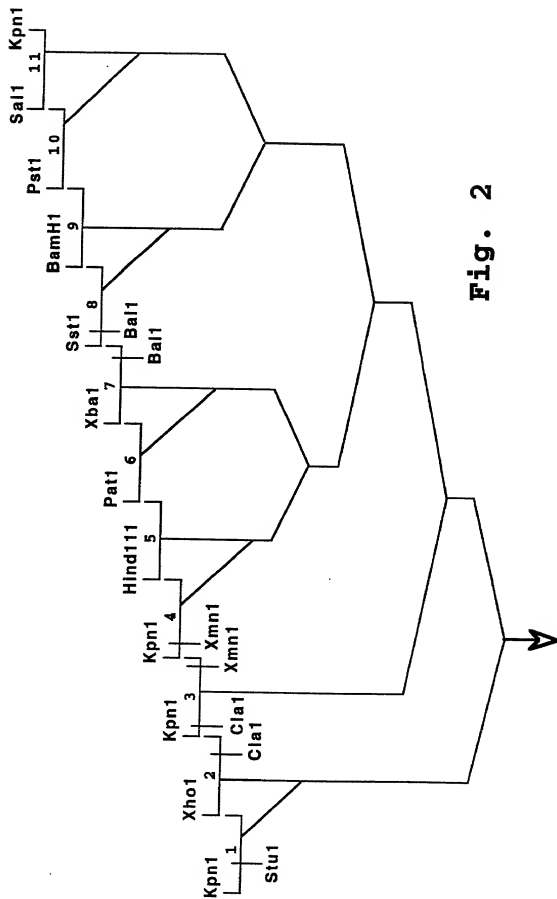


Fig. 2

```

-23                                     -9
met ala phe val leu ser leu leu met ala leu val leu val ser
oIFNt      cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
htIFN      cccc ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC

-8                                     -1 +1                                     11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT CTC
TAC GGC CCA GGA GGA TCC CTG GGT TGT GAC CTG TCT CAG AAC CAC CTG GTG GTT GGC

12                                     20                                     30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT TGT CTG
AGG AAG AAC CTC AGG CTC CTG GAC GAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG

31                                     40                                     49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
CAG GAC AGA AAA GAC TTC GCT TTA CCC CAG GAA ATG GTG GAG GGC GGC CAG CTC CAG

50                                     60                                     68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC

69 70                                     80                                     87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT
CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT

88 90                                     100                                     106
gly leu gln gln gln leu asp his leu asp thr cys arg gly gln val met gly glu
GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG
GGA CTC CAT CAG CAG CTG GAC AAC CTG GAT GCC TGC CTG GGG CAG GTG ATG GGA GAG

107 110                                     120                                     125
glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln
GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG
GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG

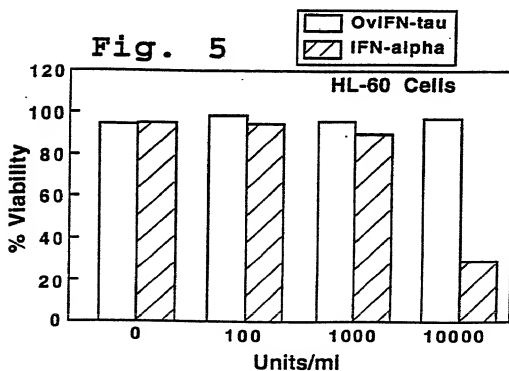
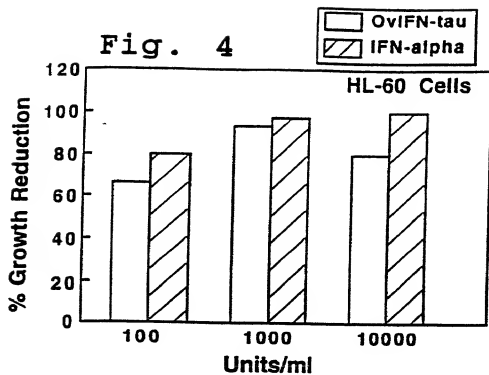
126 130                                     140                                     144
gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val
GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC
GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC

145 150                                     160                                     163
arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr
AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA
AGA CTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA AGG TTA AGA

164 172
lys met gly gly asp leu asn ser pro end
AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA
ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA

```

Fig. 3



Peptides	MW	HI*	Sequence
IFN(1-37) (SEQ ID NO:5)	4465	-0.78	CYSLRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFG
IFN(34-64) (SEQ ID NO:6)	3610	-0.72	KDFGLPQEMVEGDQLQKDAQFPVLVEMLQQS
IFN(62-92) (SEQ ID NO:7)	3586	-0.53	QQSFNLFYTEHSSAAWDTTLLQLCTGLQQQ
IFN(90-122) (SEQ ID NO:8)	3712	-0.86	QQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKK
IFN(119-150) (SEQ ID NO:9)	3948	-0.56	TVKKYFGQIVDYLOEKGYSDCAWEIVRVEMMR
IFN(139-172) (SEQ ID NO:10)	3818	-0.11	CAWEIVRVEMMRALTVSTTLQKRLTKMGGDLNSP

*Hydropathic Index

Fig. 6

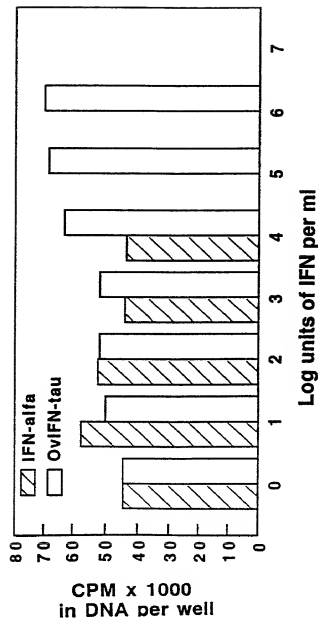


Fig. 8

1
 CTGAGATGGGATCAGAGAACCTACCTGAAGTTCCCCCTGACCCCATCTCAGCCAGCCCAGCAGCAGCCGATCTTCCCC 80
 81
 ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC TAT GGC CCA GGA 140
 S1 Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr Gly Pro Gly Gly S20
 141 TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC AGG GAG AAC CTC AAG CTC 200
 S21 Ser Leu Gly Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys Leu 17
 201 CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG CAG GAC AGA AAA GAC TTT GGT 260
 18 Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp Arg Lys Asp Phe Gly 37
 261 CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG AAG GAC CAG GCC TTC CCT GTG CTC 320
 38 Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu Gln Lys Asp Gln Ala Phe Pro Val Leu 57
 321 TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC TAC ACA GAG CAC TCC TCT GCT GCC TGG 380
 58 Tyr Glu Met Leu Gln Gln Ser Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp 77
 381 GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC 440
 78 Asp Thr Thr Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu Asp 97
 441 ACC TGC AGG GGT CAA GTG ATG GGA GAG GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT 500
 98 Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly Asn Met Asp Pro Ile 117
 501 GTG ACC GTG AAG AAG TAC TTC CAG GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC 560
 118 Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr Asp Try Leu Gln Gln Lys Gly Tyr Ser 137
 561 GAC TGC GCC TGG GAA ATC GTC AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC 620
 138 Asp Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr 157
 621 TTG CAA AAA AGG TTA ACA AAG ATG GGT GGA GAT CTG AAC TCA CCT TGATGACTCTTGCCGACTA 666
 158 Leu Gln Lys Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro 172
 764
 AGATGCCACATCAGCCCTCTACACCCGCTGTGTTTCATTTCAGAAGACTCTGATTTTCTGCTCCAGCCACCAATTTCATTG
 844
 AATTACTTTAGCTGATACTTTGTCACTAGTAAAAAGCAAGTAGATATAAAAGTATTCAGCTGTAGGGGCATGAGTCTCTGA
 924
 AATGATGCCTTCCCTGATGTTATCTGTTGCTGATTTATTATACCTTCTAGCATTTAACTACTTAAATATTAGGAAT
 972
 TTGTTAAGTTACATTACATCTGTACATCATATTAAAAAATTCTAAAAACAAAAA

Fig. 7

Fig. 9

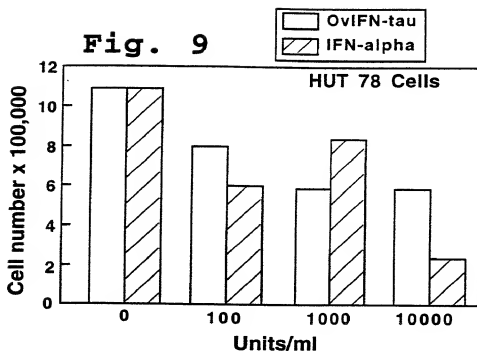


Fig. 10

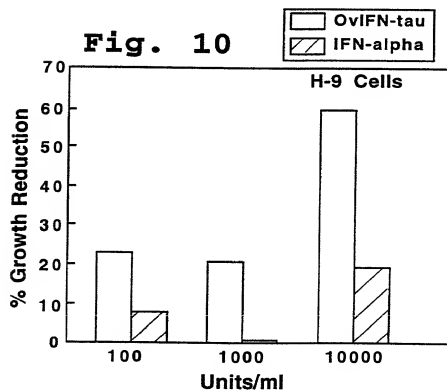


Fig. 11A

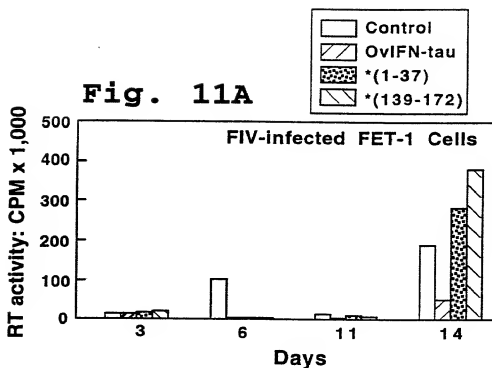


Fig. 11B

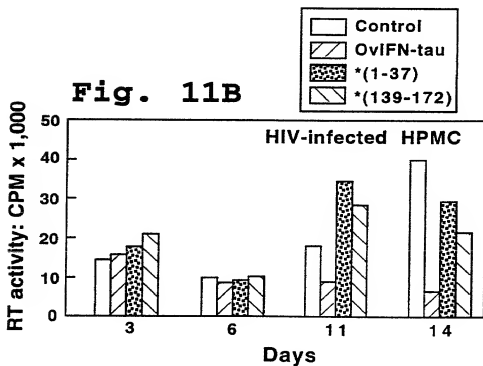


Fig. 12

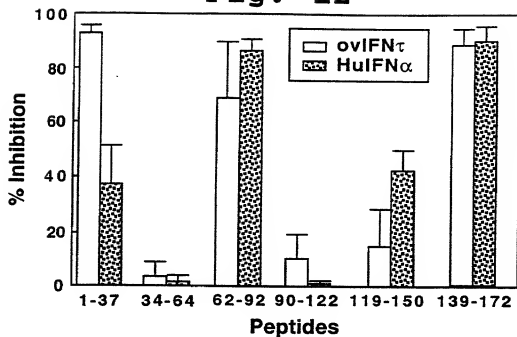


Fig. 13

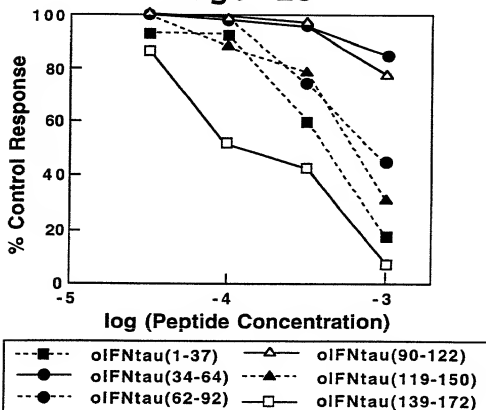
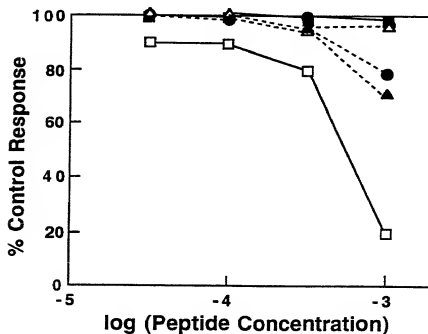
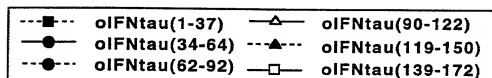
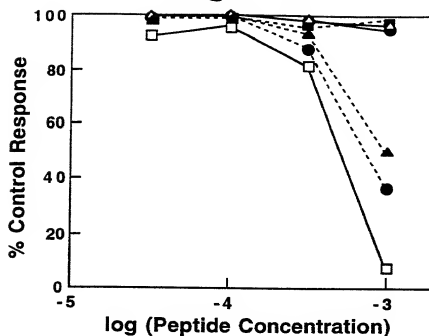


Fig. 14**Fig. 15**

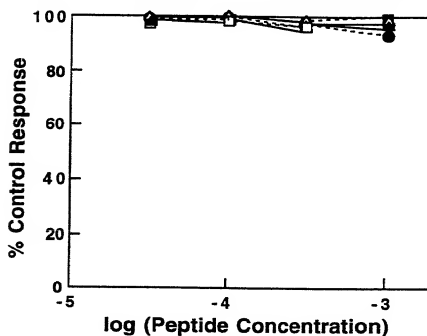
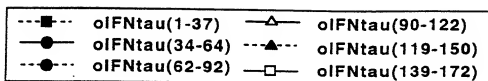


Fig. 16

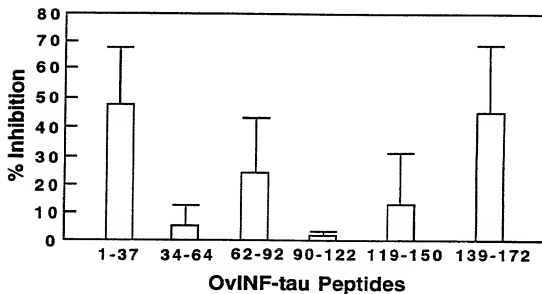
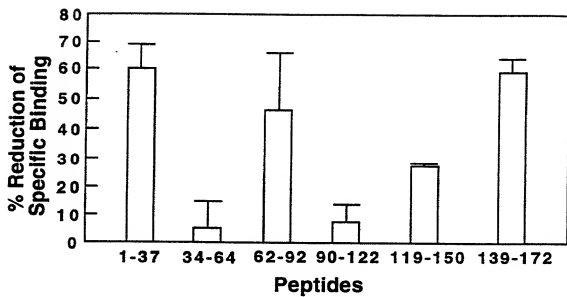


Fig. 17

**Fig. 18**


```

-23                                     -9
oINft      Met ala phe val leu ser leu leu met ala leu val leu val ser
LEXY.5      cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
TOSHI.9      cccc                                     c
TOSHI.10     cc                                     c
              cc                                     c

-8                                     -1 +1                                     11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC
c          c          c          G          A          C          A          G          T          G
c          c          c          G          A          C          A          G          T          G
c          g          c          C G          G          A          C          A          G          T          G

12                                     20                                     30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG
A          G          GA          GG          A          C          A          G          T          G
A          G          A          GG          G          C          A          G          T          G
C C          G          G          A          GG          T          GC          T

31                                     40                                     49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
c          c          t          a          a          G
c          c          t          a          TAG          a          G
c          c          t          a          TAG          a          G

Clone 21      !          t          G
Clone 35      !          t          G
Clone 15      !          t          G
Clone 18      !          T          AG          T

50                                     60                                     68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
G          C          A          T          C          T          C          T          C          T          C          T
G          C          A          T          C          T          C          T          C          T          C          T
G          C          A          T          C          T          C          T          C          T          C          T
G          C          A          T          C          T          C          T          C          T          C          T
G          C          A          T          C          T          C          T          C          T          C          T
G          C          A          T          C          T          C          T          C          T          C          T

69                                     80                                     87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT
C          C          C          C          C          C          C          C          C          C          C          C
C          C          C          C          C          C          C          C          C          C          C          C
C          C          C          C          C          C          C          C          C          C          C          C
C          C          C          C          C          C          C          C          C          C          C          C
C          C          C          C          C          C          C          C          C          C          C          C
C          A          G          G          t          t          t          t          t          t          t          t

```

Fig. 19A

88 90
 gly leu gln gln leu asp his leu asp thr cys 100 arg gly gln val met gly glu
 GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG
 T A t G CT g g
 T A t G CT g g
 T t G t G CT g g
 T t G t G CT g g
 T t G t G CT g g
 T t G t G CT g g T CT

107 110
 glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln
 GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG
 a GG C G CC C G T C G
 a GG C G CC C G T C G
 a GA C G CC C G A G t
 a GG C G CC C G A C t
 a GG C G CC C G A C t
 a GG C G CC C G GC
 a GG C G CC C G GC

126 130 140 144
 gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val
 GGC ATC TAT TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC
 C T A t t
 C T A t t
 C T A t t
 C T A t t
 C AT I
 C T I I

145 150 160 163
 arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr
 AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA
 C G a C T T T TC T T G G G
 g a C T T T TC T T G G G
 C G a C T t g T TC G C G

164 172
 lys met gly gly asp leu asn ser pro
 AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA
 T A c G
 T A c G
 T A c G

Fig. 19B

```

-23                                     -9
OTP-1      Met ala phe val leu ser leu leu met ala leu val leu val ser
LEXY.5
TOSHI.9
TOSHI.10

-8                                     -1 +1                                     11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
                                     asp gln asn his val val gly
                                     (---)asp gln asn his val val gly
                                     arg asp gln asn his val val gly

12                                     20                                     30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
  lys arg lys glu arg glu arg
  lys arg glu arg
ser gln arg gly gln arg

31                                     40                                     49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
                                     ala
                                     ala (Stop) gly
                                     ala gly
Clone 21                                     !                                     gly
Clone 35                                     !                                     gly
Clone 15                                     !                                     gly
Clone 18                                     !                                     val ser phe

50                                     60                                     68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
glu ala ile ser his
glu ala ile ser his
glu ala ile ser his
glu ala ile ser his
glu ala ile ser his
glu ala ile ser his lys
glu ala ile ser his

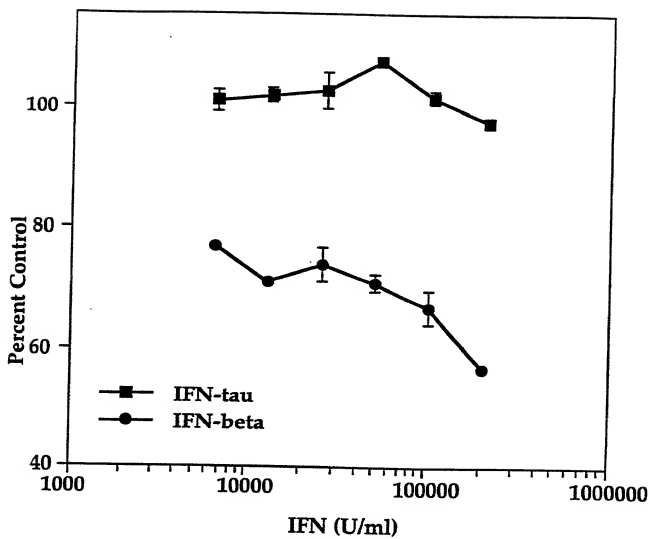
69                                     80                                     87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
his arg
his arg
his arg
his arg
his arg
his lys arg
his lys arg leu

```

Fig. 20A

[illegible]

Fig. 20B

**Fig. 21**